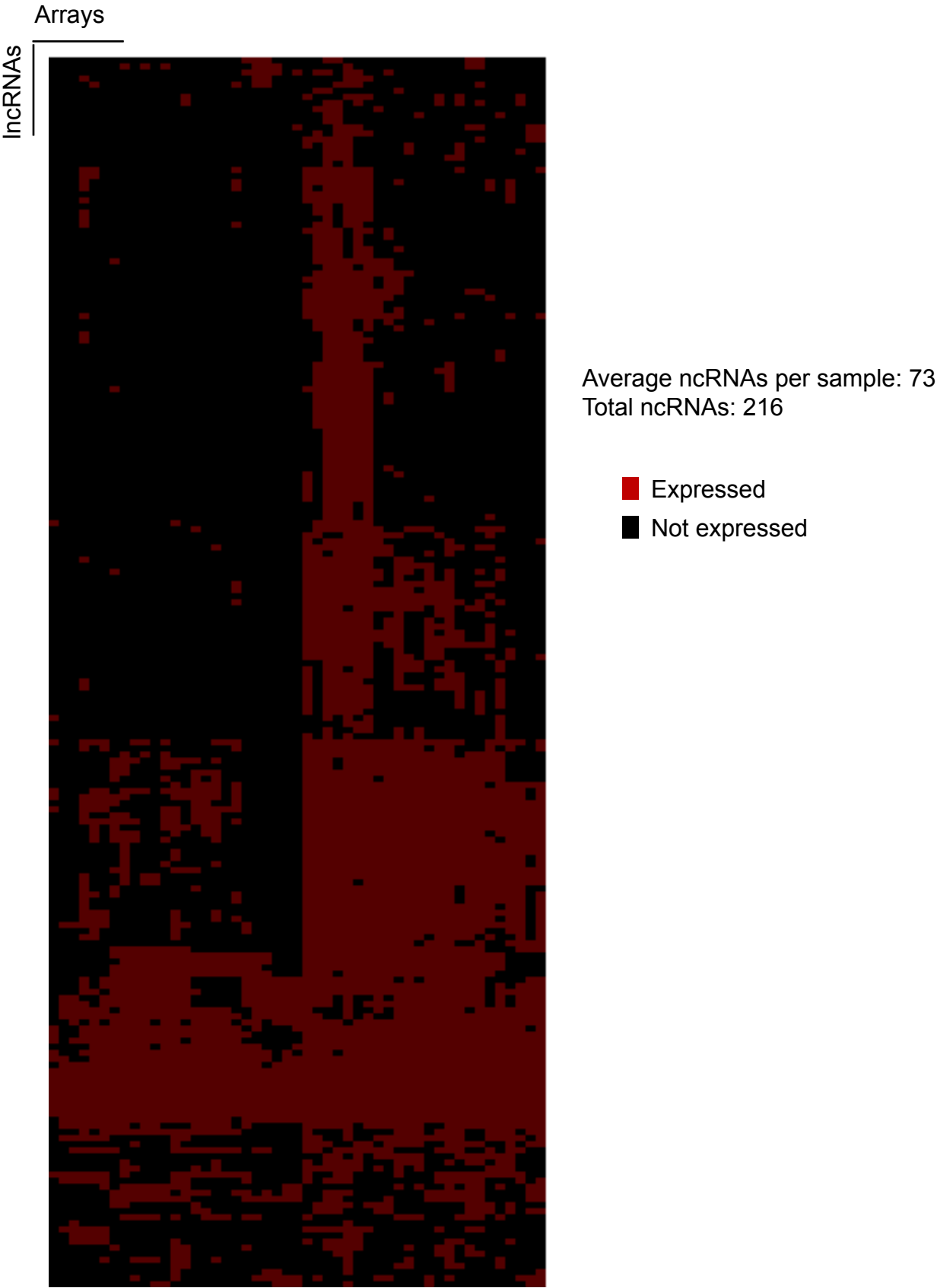


## **Supplementary Data:**

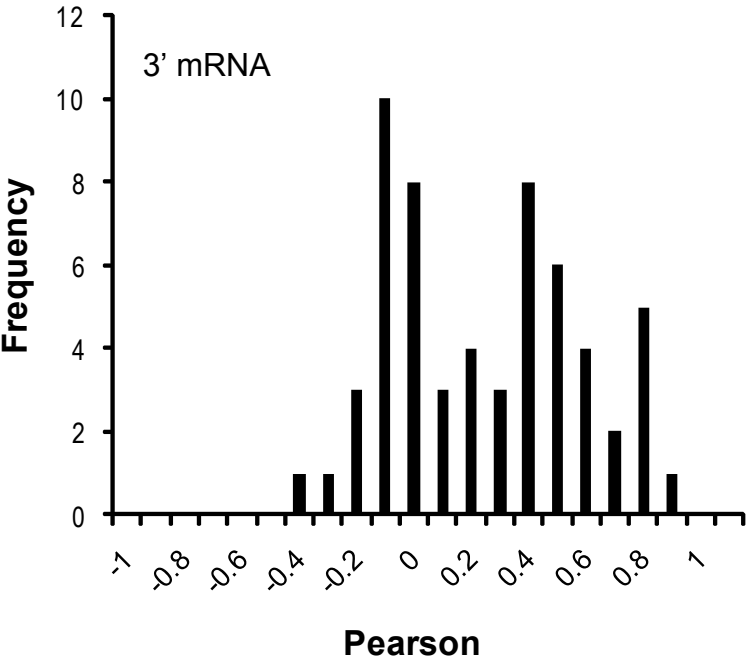
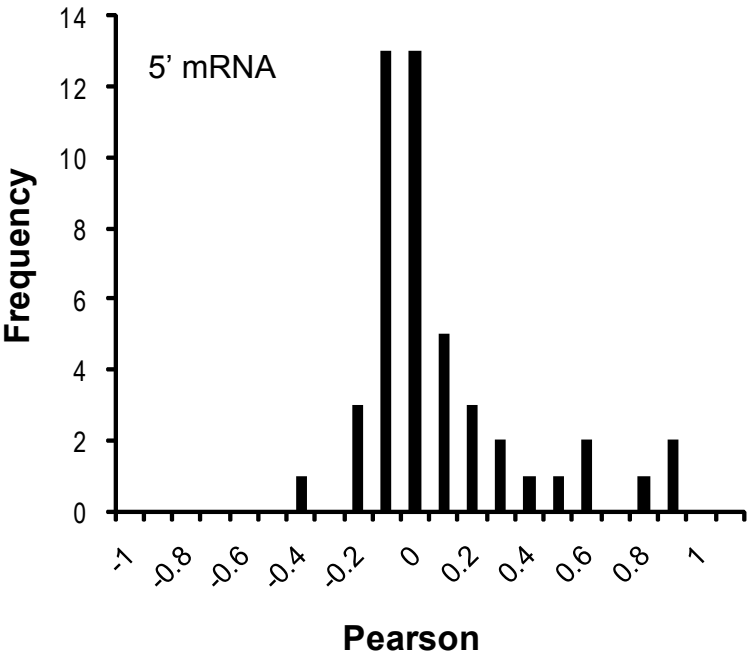
### **Extensive and coordinated transcription of noncoding RNAs within cell cycle promoters**

Tiffany Hung<sup>1,2</sup>, Yulei Wang<sup>3</sup>, Michael F. Lin<sup>4,5</sup>, Ashley K. Koegel<sup>1,2</sup>, Yojiro Kotake<sup>6-8</sup>, Gavin Grant<sup>9</sup>, Hugo M. Horlings<sup>10</sup>, Nilay Shah<sup>11</sup>, Christopher Umbricht<sup>12</sup>, Pei Wang<sup>13</sup>, Yu Wang<sup>3</sup>, Benjamin Kong<sup>3</sup>, Anita Langerod<sup>14,15</sup>, Seung K. Kim<sup>2,13</sup>, Marc van de Vijver<sup>10</sup>, Saraswati Sukumar<sup>11</sup>, Michael L. Whitfield<sup>9</sup>, Manolis Kellis<sup>4,5</sup>, Yue Xiong<sup>6</sup>, David J. Wong<sup>1\*</sup>, Howard Y. Chang<sup>1,2\*</sup>

**Supplementary Figure 1.** Heatmap of lncRNAs expressed in each of the 104 different RNA tiling arrays as determined by peak calling analysis (see Methods).

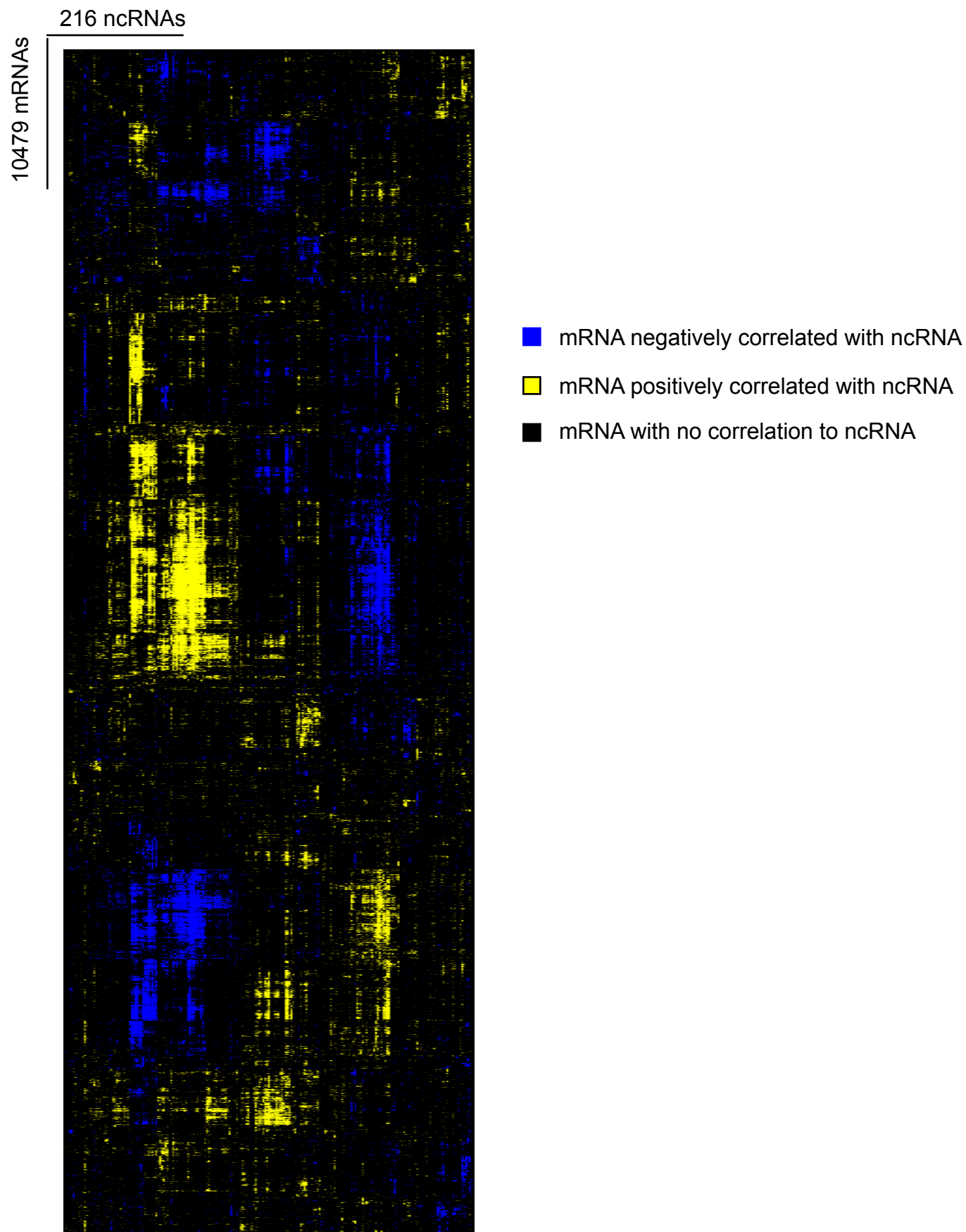


**Supplementary Figure 2.** RT-PCR validated expression correlation between 60 lncRNAs and their nearest 3' and 5' mRNAs across 34 RNA samples.

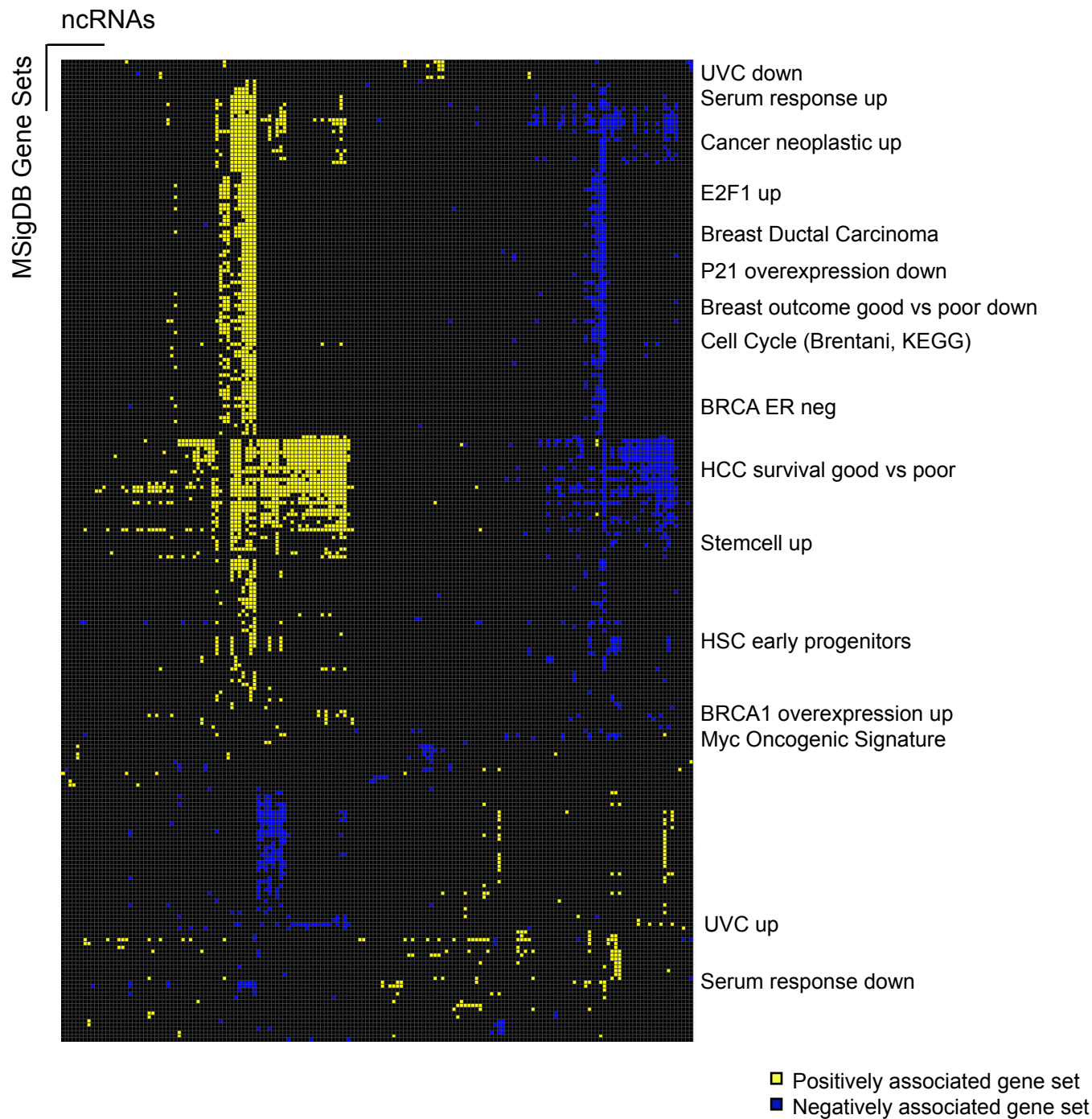


### Supplementary Figure 3.

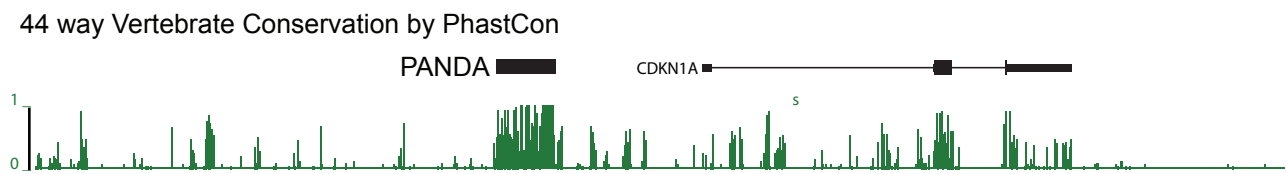
Gene sets of mRNAs positively or negatively correlated with each lncRNA as determined by pairwise Pearson correlation across 17 tiling and expression arrays.



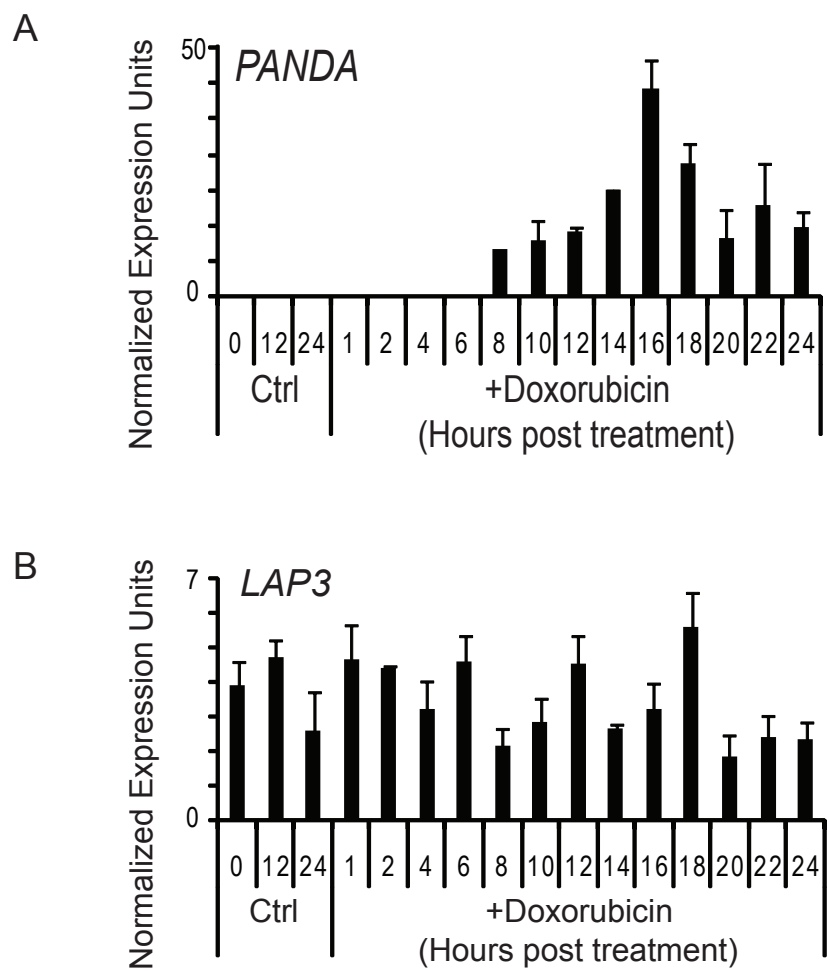
**Supplementary Figure 4.** Molecular Signature Data Base module map of gene sets associated with lncRNAs.



**Supplementary Figure 5.** PANDA is evolutionarily conserved across vertebrates as determined by 44 way Vertebrate Conservation PhastCon score.



**Supplementary Figure 6.** 24 hour DNA damage time course of PANDA and LAP3 expression. Human fetal lung fibroblasts (FL3) cells were treated with doxorubicin and collected at the indicated time points for RT-PCR analysis.



**Supplementary Figure 7.** RLM-RACE sequence of PANDA

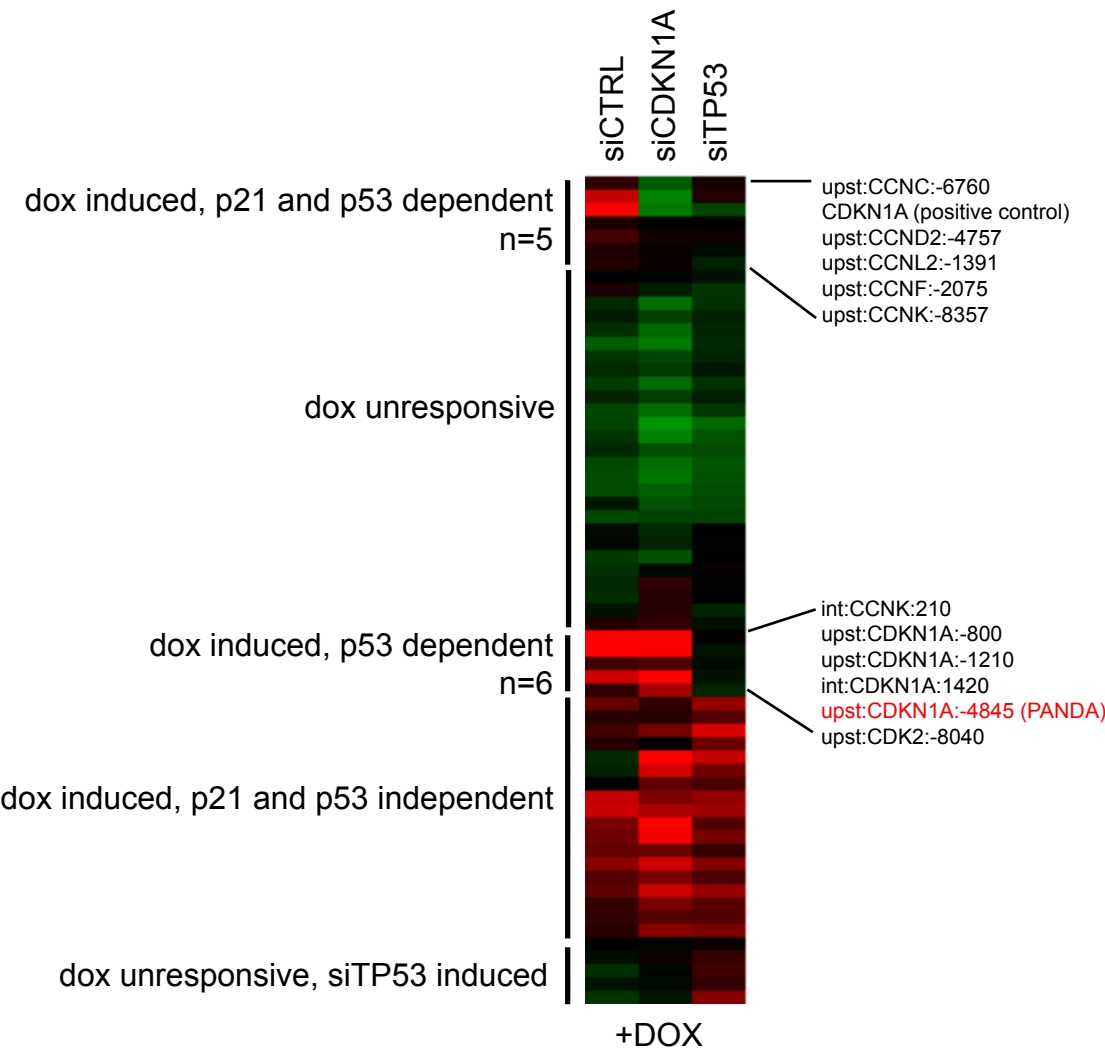
**A.** 5'RACE sequence of PANDA

TAGATGTAGCTTTGGGGTCAGGTGCCACTGGGGTCTTTACCAATTCATCCTGGCTCTGGAACAAGCTC  
TTCGAGGCCAGCATTGAAACAGGGGACCGTGTCTGGAGGATGCCTCTCTTCAAACATTGTACAAGAC  
AGGTTGTAGATTGCCAGCTGGCTGATATTAACAACATTGGAAAATATAGATCTGCGGGAGCATGTACAT  
CTGCGGCATTCCTGAAAGAATTCGT

**B.** 3' RACE sequence of PANDA

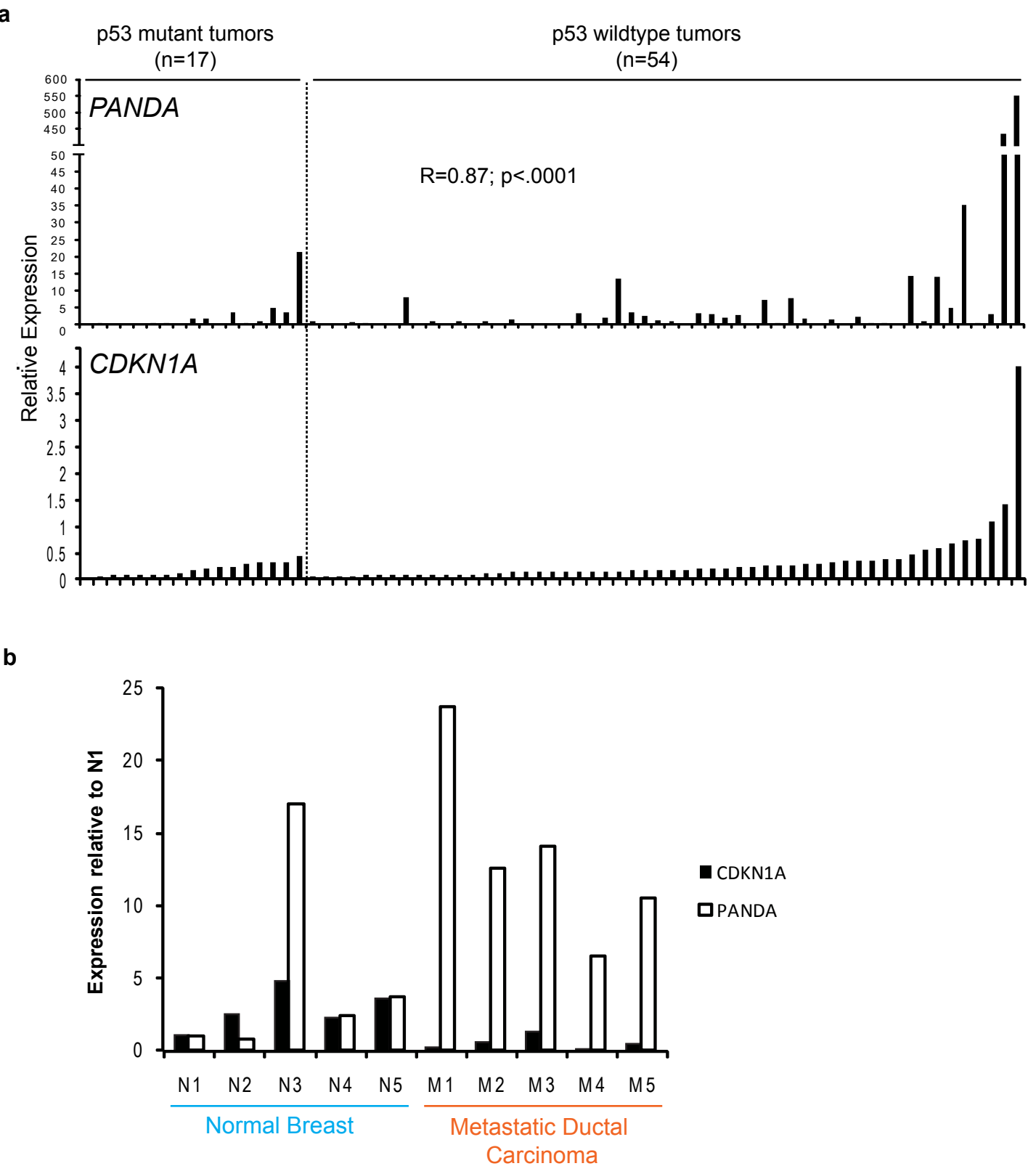
TCATAGAGACCAAGCACCGCGCCCTCCTCAGCAGCCTGAGCATCTCTACAGGGATCCACCTCCACGGA  
AGAGAGCTCCAGGTCTTGAATCTGCCTGCATCCTGCTGCAACAGCAGCTCTGATGTTTTCTTTGCCTTC  
CTGCCAGTTTTCTGTTCGTCGATTCTGGCTGCCTTTTTGCCGAGGCCAACTAGCACCCACGCTGGGGAA  
GTCCTGATGCAGACCATAAAAGGTTTCGAGTCTTGCCTGCCTTCAGAGGTGGTCCAGATATGTTCAAAGT  
CTCTCTCAGCTTTCCAGCTATCAATTTATCAAGATTCTCTCCTGCACTTGTGAACTGTGGCACATCATCTT  
CTTTTTCTTTGGAATAGATTCCTAAAACAAGGCCCTTCGTCATGTCTGCAGCGGAGAGACCCCGGCTCC  
CGAAACATCTCACGGCCAGACGTCAGACGATGACTCGCCCCACCCAATGTTTGTATTTTAGTAGAGAGA  
GGGTTTCTCTATGTTGGTCAGGCTGGTCTCAAACCTCGACCTCAGTTGATCTGTCTGCCTCGGTCTCCCA  
AAGTGCTGAGATTACAGGCGTGAGCCACTGC

**Supplementary Figure 8.** p53-dependent DNA damage induction in a subset of lncRNAs. Heatmap of lncRNA expression (as measured by RT-PCR) of human fetal lung fibroblasts (FL3) treated with doxorubicin in the presence of siCTRL, siCDKN1A, or siTP53. Red indicates induction relative to undamaged cells, green indicates repression.



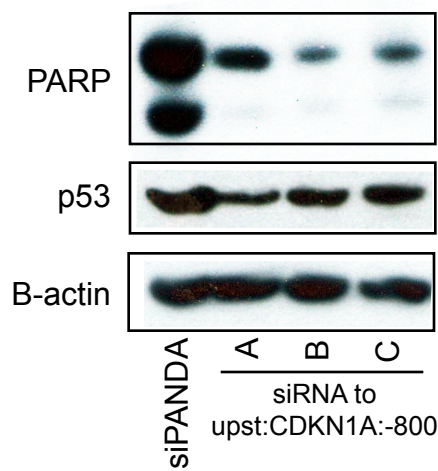


**Supplementary Figure 9.** PANDA expression level in tumors. (A) Expression in p53 mutant vs. p53 wildtype tumors. Human primary breast tumors were derived from the fresh-frozen tissue bank of the Netherlands Cancer Institute/Antoni van Leeuwenhoek Hospital . For mutational analysis, DNA extraction was performed as described previously<sup>1</sup> and TP53 mutations were identified by DNA sequencing for exons 2-11 as described<sup>2</sup>. (B) Expression of PANDA in 5 normal breast tissues vs. 5 metastatic ductal carcinomas, also obtained from the same tissue depository as (A).

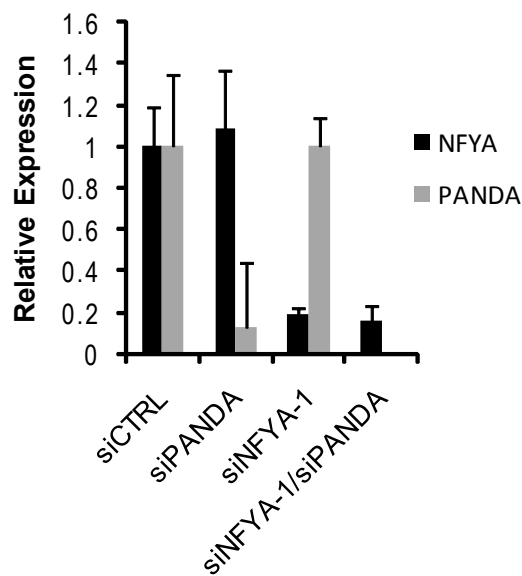


1. Horlings, H.M. et al. Integration of DNA copy number alterations and prognostic gene expression signatures in breast cancer patients. *Clin Cancer Res* 16, 651-63.

**Supplementary Figure 10.** Three independent siRNAs to upst:CDKN1A:-800 did not induce PARP cleavage in FL3 cells upon treatment with doxorubicin.



**Supplementary Figure 11.** Knockdown efficiency of NFYA and PANDA for Fig 7d and 7e.



Supplementary Table 1: Tiling Array design

<u>Name</u>	<u>Chromosome</u>	<u>Feature Coordinates (Human March 2006 NCBI Build 36.1 hg18)</u>
9p21 locus	9	21900000-22150000
CCNA1	13	35894632-35906659
CCNA2	4	122962330-122974342
CCNB1	5	68488668-68500750
CCNB2	15	57174611-57186627
CCNB3	X	50034275-50046275
CCNC	6	100121225-100133411
CCND1	11	69155053-69167126
CCND2	12	4243198-4255223
CCND3	6	42015122-42027530
CCNE1	19	34984740-34997400
CCNE2	8	95974605-95986660
CCNF	16	2409440-2421471
CCNG1	5	162787154-162799204
CCNG2	4	78287401-78299550
CCNH	5	86742441-86754592
CCNI	4	78214148-78226149
CCNJ	10	97783140-97795329
CCNJL	5	159697177-159709177
CCNK	14	99007491-99019512
CCNL1	3	158358577-158371176
CCNL2	1	1322552-1334571
CCNO	5	54563265-54575265
CCNT1	12	47395048-47407048
CCNT2	2	135382862-135394875
CCNY	10	35565959-35577959
CCNYL1	2	208274509-208286509
CCNYL2	10	42268168-42280168
CCNYL3	16	34105360-34117360
CDK2	12	54636825-54648899
CDK3	17	71499013-71511013
CDK4	12	56430344-56442431
CDK5	7	150383893-150395929
CDK5R1	17	27828217-27840681
CDK5R2	2	219522620-219534641
CDK6	7	92299148-92311148
CDK8	13	25716755-25728778
CDK9	9	129578151-129590188
CDK10	16	88270578-88282613
CDKL1	14	49930367-49942367
CDKL2	4	76772269-76784595
CDKL3	5	133728113-133740664
CDKL4	2	39308177-39320177
CDKL5	X	18343677-18355677
CDKN1A	6	36744464-36756493
CDKN1B	12	12751575-12763663
CDKN1C	11	2861551-2873577
CDKN2C	1	51196148-51210203
CDKN2D	19	10538631-10550655
CDKN3	14	53923462-53935475

CNNM1	10 101070022-101082022
CNNM2	10 104658064-104670853
CNNM3	2 96835714-96848658
CNNM4	2 96780365-96792606

**Hung et al., Supplementary Table 2**

<u>Sample pair #</u>	<u>Experimental sample</u>
1	Human fetal lung fibroblasts treated with doxorubicin (200ng/ul) for 24 hours
2	Human fetal lung fibroblasts in low serum (0.01%)
3	Human fetal lung fibroblasts transduced with HPV-E7
4	Human fetal lung fibroblasts transduced with HPV-E6
5	Human fetal lung fibroblasts transduced with HRAS
6	HeLa synchronized by double thymidine block: 0 hr
7	HeLa synchronized by double thymidine block: 2 hr
8	HeLa synchronized by double thymidine block: 4 hr
9	HeLa synchronized by double thymidine block: 6 hr
10	HeLa synchronized by double thymidine block: 8 hr
11	HeLa synchronized by double thymidine block: 10 hr
12	HeLa synchronized by double thymidine block: 12 hr
13	Primary human keratinocytes transduced with p63 shRNA
14	Primary human keratinocytes treated with Ca2+ for 48 hours
15	U2OS synchronized by double thymidine block: 0 hr
16	U2OS synchronized by double thymidine block: 2 hr
17	U2OS synchronized by double thymidine block: 4 hr (A)
18	U2OS synchronized by double thymidine block: 4 hr (B)
19	U2OS synchronized by double thymidine block: 6 hr
20	U2OS synchronized by double thymidine block: 8 hr
21	U2OS synchronized by double thymidine block: 14 hr
22	U2OS synchronized by double thymidine block: 16 hr
23	Human ES (H9)
24	Human ES (H9)
25	Human ES (H9)
26	MCF7 cell line
27	Primary human keratinocytes transduced with MYC
28	Primary human keratinocytes transduced with MYC
29	Primary human keratinocytes transduced with HRAS
30	Primary human keratinocytes transduced with HRAS
31	Primary human keratinocytes transduced with E2F3
32	Primary human keratinocytes transduced with E2F3
33	Primary human keratinocytes transduced with Ikb
34	Primary human keratinocytes transduced with Ikb
35	Primary human keratinocytes transduced with MYC, RAS, and Ikb
36	Primary human keratinocytes transduced with MYC, RAS, and Ikb
37	Primary human keratinocytes transduced with E2F3, RAS, and Ikb
38	Primary human keratinocytes transduced with E2F3, RAS, and Ikb
39	Primary human keratinocytes transduced with SOX2, RAS, and Ikb
40	Primary human keratinocytes transduced with SOX2, RAS, and Ikb
41	MYC-RAS-Ikb tumor 1
42	MYC-RAS-Ikb tumor 2
43	E2F3-RAS-Ikb tumor 1
44	E2F3-RAS-Ikb tumor 2
45	Invasive ductal breast carcinoma P2
46	Invasive ductal breast carcinoma P3
47	Invasive ductal breast carcinoma P4
48	Invasive ductal breast carcinoma P5
49	Invasive ductal breast carcinoma P6
50	Invasive ductal breast carcinoma P7
51	Invasive ductal breast carcinoma P9
52	Invasive ductal breast carcinoma P10

[illegible]

## Supplementary Table 5

### Primers and Oligos

#### RACE primers for PANDA

Fwd	5'-CAGAACTTGGCATGATGGAG-3'
Rev	5'-TGATATGAAACTCGGTTTACTACTAGC-3'
Fwd2	5'-TGCACACATTTAACCCGAAG-3'
Rev2	5'-CCCCAAAGCTACATCTATGACA-3'
Rev3	5'-CGTCTCCATCAT GCCAAGTT-3'
Rev4	5'-CATAGAGCTTCACCGACATAGC-3'

#### RT-PCR primers for PANDA

Fwd	5'-TGCACACATTTAACCCGAAG-3'
Rev	5'-CCCCAAAGCTACATCTATGACA-3'

#### siRNAs for PANDA

siRNA pool A	5'-AAUGUGUGCACGUAACAGAUU-3' 5'-GAGAUUUGCAGCAGACACAUU-3'
siRNA pool B	5'-GGGCAUGUUUUCACAGAGGUU-3' 5'-GAGAUUUGCAGCAGACACAUU-3'
siRNA pool C	5'-AAUGUGUGCACGUAACAGAUU-3' 5'-GGGCAUGUUUUCACAGAGGUU-3'
siCTRL	Dharmacon D-001810-10

#### siRNAs for mRNAs

siNFYA pool	si9530 Ambion si9529 Ambion si9528 Ambion
siTP53	S606 Ambion
siCDKN1A	S417 Ambion

#### Chip primers

PUMA fwd	5'-CGT GGA TTC CTG TCT CCT CT-3'
PUMA rev	5'-GTC ACT CTG GTG AGG CGA TT-3'
NOXA fwd	5'-TTT CCC TTC CCT GTT ACT GC-3'
NOXA rev	5'-CTT GGG TAA ACA AGC CCA GA-3'

#### Taqman assays

<i>PANDA</i>	custom Taqman
<i>TP53</i>	Hs99999147_m1
<i>LAP3</i>	Rh02870758_m1
<i>APAF1</i>	Hs00559441_m1
<i>LRDD</i>	Hs00388035_m1

<i>FAS</i>	Hs00163653_m1
<i>BIK</i>	Hs00154189_m1
<i>CDKN1A</i>	Hs01121168_m1
<i>GAPDH</i>	Hs99999905_m1